SEQUENCE LISTING

<110> Tao, Yumin
      Gordon-Kamm William J.
      Lowe, Keith S.
      Bailey, Matthew A.

<120> Cell Cycle Polynucleotide, Polypeptide,
  and Uses Thereof

<130> 1109

<150> US 60/119,857
<151> 1999-02-12

<150> US 60/101,551
<151> 1998-09-23

<150> US 09/398,858
<151> 1999-09-20

<150> US 09/257,131
<151> 1999-02-25

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tcacggggct cctccgtccg taaggcaccg ccgcagcgtc tcggctggat caacaggccg   60
gccgatccgt cttcttcccc tcctcctgcg ggtcggcgtt tggggatc atg gcg gcg   117
                                                      Met Ala Ala
                                                        1

cgg gcg gct gac gag aac agg aga ccg gcg gca ggg aag ccc gcg cca   165
Arg Ala Ala Asp Glu Asn Arg Arg Pro Ala Ala Gly Lys Pro Ala Pro
    5   10   15

ggc gtc cga gac atg gcg agc cgg cgc gcg ctc acg gac atc aag aac   213
Gly Val Arg Asp Met Ala Ser Arg Arg Ala Leu Thr Asp Ile Lys Asn
 20   25   30   35

ctc gtc ggg gct gcc ccg tac ccc tac gcc gtc gcc aag aag ccc atg   261
Leu Val Gly Ala Ala Pro Tyr Pro Tyr Ala Val Ala Lys Lys Pro Met
             40   45   50

ctg cag aag agc aaa agg gac gaa aag cag cca gcg ttg gca agc agc   309
Leu Gln Lys Ser Lys Arg Asp Glu Lys Gln Pro Ala Leu Ala Ser Ser

1

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cgg ccc atg aca agg aaa ttc gcc gcc tcc ttg gcg agc aag ggc caa        357
Arg Pro Met Thr Arg Lys Phe Ala Ala Ser Leu Ala Ser Lys Gly Gln
        70                  75                  80

cct gaa tgt cag ccg atc gta gct gat cca gaa ccc gaa gtt tgt caa        405
Pro Glu Cys Gln Pro Ile Val Ala Asp Pro Glu Pro Glu Val Cys Gln
        85                  90                  95

cag aag gaa tca gta ggc gat ggc acc gtt gat att gac gtg gaa ctc        453
Gln Lys Glu Ser Val Gly Asp Gly Thr Val Asp Ile Asp Val Glu Leu
100                 105                 110                 115

tac gag ctg gtc gac ggt agt gat agt gac atc gac atg ggt gcg aca        501
Tyr Glu Leu Val Asp Gly Ser Asp Ser Asp Ile Asp Met Gly Ala Thr
                120                 125                 130

gag aac aag gac att atg aac gaa gat gaa ttg ctc atg gat att gac        549
Glu Asn Lys Asp Ile Met Asn Glu Asp Glu Leu Leu Met Asp Ile Asp
                135                 140                 145

agt gca gac tcg ggg aac ccg ctt gct gca aca gaa tat gtt aaa gag        597
Ser Ala Asp Ser Gly Asn Pro Leu Ala Ala Thr Glu Tyr Val Lys Glu
                150                 155                 160

ctt tac acc ttt tac aga gaa aat gag gct aag agt tgt gta agg cca        645
Leu Tyr Thr Phe Tyr Arg Glu Asn Glu Ala Lys Ser Cys Val Arg Pro
        165                 170                 175

gat tac atg tcc agc caa caa gac ata aac tca aag atg aga gca att        693
Asp Tyr Met Ser Ser Gln Gln Asp Ile Asn Ser Lys Met Arg Ala Ile
180                 185                 190                 195

ctg att gac tgg ctg att gag gtt cac tac aag ttt gaa ctg atg gat        741
Leu Ile Asp Trp Leu Ile Glu Val His Tyr Lys Phe Glu Leu Met Asp
                200                 205                 210

gag acg ctc ttt ctt atg gta aac ata ata gat aga ttc ttg gaa aag        789
Glu Thr Leu Phe Leu Met Val Asn Ile Ile Asp Arg Phe Leu Glu Lys
                215                 220                 225

gaa gtg gtt cca agg aag aag cta caa ctg gtt gga gtc aca gct atg        837
Glu Val Val Pro Arg Lys Lys Leu Gln Leu Val Gly Val Thr Ala Met
        230                 235                 240

ctg ctc gct tgt aaa tat gag gag gta tct gtt cca gtt gtt gag gac        885
Leu Leu Ala Cys Lys Tyr Glu Glu Val Ser Val Pro Val Val Glu Asp
        245                 250                 255

ctt gtg ctg ata tct gac cgt gcc tac aca aaa ggg caa att tta gaa        933
Leu Val Leu Ile Ser Asp Arg Ala Tyr Thr Lys Gly Gln Ile Leu Glu
260                 265                 270                 275

atg gaa aag ttg att ctg aac acg ctg cag ttc aac atg tct gtt cca        981
Met Glu Lys Leu Ile Leu Asn Thr Leu Gln Phe Asn Met Ser Val Pro
                280                 285                 290

aca cct tat gtc ttc atg aag agg ttt ctg aaa gct gca gat gca gat        1029
Thr Pro Tyr Val Phe Met Lys Arg Phe Leu Lys Ala Ala Asp Ala Asp
                295                 300                 305
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2

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aaa cag ctt gag cta gcg tca ttt ttc atg ctg gag ctc tgc ttg gta        1077
Lys Gln Leu Glu Leu Ala Ser Phe Phe Met Leu Glu Leu Cys Leu Val
        310             315             320

gaa tac caa atg ctg aat tat cgg cct tcg cat ctg gct gct gct gcg        1125
Glu Tyr Gln Met Leu Asn Tyr Arg Pro Ser His Leu Ala Ala Ala Ala
325             330             335

gtt tat act gca cag tgt gct atc aat cgt tgc cag cac tgg aca aag        1173
Val Tyr Thr Ala Gln Cys Ala Ile Asn Arg Cys Gln His Trp Thr Lys
340             345             350             355

gtc tgc gag tct cat agc aga tac act agc gac caa ctc ctg gag tgc        1221
Val Cys Glu Ser His Ser Arg Tyr Thr Ser Asp Gln Leu Leu Glu Cys
                360             365             370

tcg agg atg atg gta gat ttt cac cag aag gct gga acc agt aag ctc        1269
Ser Arg Met Met Val Asp Phe His Gln Lys Ala Gly Thr Ser Lys Leu
                375             380             385

act ggc gtg cac agg aag tac agt acc tac aag ttc ggt tgc gtg gcc        1317
Thr Gly Val His Arg Lys Tyr Ser Thr Tyr Lys Phe Gly Cys Val Ala
                390             395             400

aag att ttg cct gcg cag ttc ctg ctg gag tcg gga ggg aca ccg cct        1365
Lys Ile Leu Pro Ala Gln Phe Leu Leu Glu Ser Gly Gly Thr Pro Pro
        405             410             415

cct tca ggt gca aac t agttgaatcg acctattcaa ctgggtggat ttttaaagt      1421
Pro Ser Gly Ala Asn
420

ttttagaata ctccatgaac aagatgcaga aaacatcgtg ttgatgttgc ccaaaagtgc      1481
atcgaatttc tttggagagt tatgattaac aacttttttt ttatctatgt tgaatgacga      1541
gtgacggtcg gtcacgttgt gcttgtgcag ttatactgcg gctaataaca aactgtccag      1601
ttnttctnaa aaaaaaaaaa aaaaaaaaaa aaaaa                                  1636
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Pro Ala Pro Gly Val Arg Asp Met Ala Ser Arg Arg Ala Leu Thr Asp
            20   25   30
Ile Lys Asn Leu Val Gly Ala Ala Pro Tyr Pro Tyr Ala Val Ala Lys
        35   40   45
Lys Pro Met Leu Gln Lys Ser Lys Arg Asp Glu Lys Gln Pro Ala Leu
    50   55   60
Ala Ser Ser Arg Pro Met Thr Arg Lys Phe Ala Ala Ser Leu Ala Ser
65   70   75   80
Lys Gly Gln Pro Glu Cys Gln Pro Ile Val Ala Asp Pro Glu Pro Glu
                85   90   95
Val Cys Gln Gln Lys Glu Ser Val Gly Asp Gly Thr Val Asp Ile Asp
            100   105   110
Val Glu Leu Tyr Glu Leu Val Asp Gly Ser Asp Ser Asp Ile Asp Met
        115   120   125
Gly Ala Thr Glu Asn Lys Asp Ile Met Asn Glu Asp Glu Leu Leu Met
    130   135   140
Asp Ile Asp Ser Ala Asp Ser Gly Asn Pro Leu Ala Ala Thr Glu Tyr

3

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      145                    150                    155                    160
      Val Lys Glu Leu Tyr Thr Phe Tyr Arg Glu Asn Glu Ala Lys Ser Cys
                      165                    170                    175
      Val Arg Pro Asp Tyr Met Ser Ser Gln Gln Asp Ile Asn Ser Lys Met
                      180                    185                    190
      Arg Ala Ile Leu Ile Asp Trp Leu Ile Glu Val His Tyr Lys Phe Glu
                      195                    200                    205
      Leu Met Asp Glu Thr Leu Phe Leu Met Val Asn Ile Ile Asp Arg Phe
          210                    215                    220
      Leu Glu Lys Glu Val Val Pro Arg Lys Lys Leu Gln Leu Val Gly Val
      225                    230                    235                    240
      Thr Ala Met Leu Leu Ala Cys Lys Tyr Glu Glu Val Ser Val Pro Val
                      245                    250                    255
      Val Glu Asp Leu Val Leu Ile Ser Asp Arg Ala Tyr Thr Lys Gly Gln
                      260                    265                    270
      Ile Leu Glu Met Glu Lys Leu Ile Leu Asn Thr Leu Gln Phe Asn Met
                      275                    280                    285
      Ser Val Pro Thr Pro Tyr Val Phe Met Lys Arg Phe Leu Lys Ala Ala
          290                    295                    300
      Asp Ala Asp Lys Gln Leu Glu Leu Ala Ser Phe Phe Met Leu Glu Leu
      305                    310                    315                    320
      Cys Leu Val Glu Tyr Gln Met Leu Asn Tyr Arg Pro Ser His Leu Ala
                      325                    330                    335
      Ala Ala Ala Val Tyr Thr Ala Gln Cys Ala Ile Asn Arg Cys Gln His
                      340                    345                    350
      Trp Thr Lys Val Cys Glu Ser His Ser Arg Tyr Thr Ser Asp Gln Leu
                      355                    360                    365
      Leu Glu Cys Ser Arg Met Met Val Asp Phe His Gln Lys Ala Gly Thr
          370                    375                    380
      Ser Lys Leu Thr Gly Val His Arg Lys Tyr Ser Thr Tyr Lys Phe Gly
      385                    390                    395                    400
      Cys Val Ala Lys Ile Leu Pro Ala Gln Phe Leu Leu Glu Ser Gly Gly
                      405                    410                    415
      Thr Pro Pro Pro Ser Gly Ala Asn
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        <213> Artificial Sequence

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gctaagagtt gtgtaaggcc ag
22
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4

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ttgggcaaca tcaacacgat g
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<210> 6
<211> 23
<212> DNA
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<220>
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<222> (1)...(23)

<400> 6
aacccgcttg ctgcaacaga ata
23


<210> 7
<211> 23
<212> DNA
<213> articifial organism

<220>
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<222> (1)...(23)

<400> 7
aatccaccca gttgaatagg tcg
23


<210> 8
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<222> (1)...(23)

<400> 8
atccgtcttc ttcccctcct cct
23
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